Validated By CRFValidator v 1.0.3

Application No: 10569000   Version No: 4.0

Input Set:

Output Set:

Started: 2011-03-01 18:47:41.474
Finished: 2011-03-01 18:47:45.877
Elapsed: 0 hr(s) 0 min(s) 4 sec(s) 403 ms
Total Warnings: 1
Total Errors: 0
No. of SeqIDs Defined: 44
Actual SeqID Count: 44

Error code   Error Description

W   213   Artificial or Unknown found in <213> in SEQ ID (44)

SEQUENCE LISTING

<110>   University of Florida Research Foundation, Inc.
         Hannah, L. Curtis
         Lyerly Linebarger, Carla R.

<120>   Heat Stable Variants of Adenosine Diphosphate Glucose
         Pyrophosphorylase

<130>   UF.371XC1

<140>   10569000
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<151>   2004-08-18

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<170>   PatentIn version 3.5

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Thr Ala Ala Glu Gln Pro Ile Pro Lys Arg Asp Lys Ala Ala Ala Asn
                20   25   30

Asp Ser Thr Tyr Leu Asn Pro Gln Ala His Asp Ser Val Leu Gly Ile
        35   40   45

Ile Leu Gly Gly Gly Ala Gly Thr Arg Leu Tyr Pro Leu Thr Lys Lys
    50   55   60

Arg Ala Lys Pro Ala Val Pro Leu Gly Ala Asn Tyr Arg Leu Ile Asp
65   70   75   80

Ile Pro Val Ser Asn Cys Leu Asn Ser Asn Ile Ser Lys Ile Tyr Val
                85   90   95

Leu Thr Gln Phe Asn Ser Ala Ser Leu Asn Arg His Leu Ser Arg Ala
            100   105   110

Tyr Gly Ser Asn Ile Gly Gly Tyr Lys Asn Glu Gly Phe Val Glu Val
        115   120   125

Leu Ala Ala Gln Gln Ser Pro Asp Asn Pro Asn Trp Phe Gln Gly Thr
    130   135   140

Ala Asp Ala Val Arg Gln Tyr Leu Trp Leu Phe Glu Glu His Asn Val
145   150   155   160

Met Glu Phe Leu Ile Leu Ala Gly Asp His Leu Tyr Arg Met Asp Tyr
                165   170   175

Glu Lys Phe Ile Gln Ala His Arg Glu Thr Asn Ala Asp Ile Thr Val
                180   185   190

Ala Ala Leu Pro Met Asp Glu Lys Arg Ala Thr Ala Phe Gly Leu Met
        195   200   205

Lys Ile Asp Glu Glu Gly Arg Ile Ile Glu Phe Ala Glu Lys Pro Lys
        210   215   220

Gly Glu Gln Leu Lys Ala Met Met Val Asp Thr Thr Ile Leu Gly Leu
225   230   235   240

Asp Asp Val Arg Ala Lys Glu Met Pro Tyr Ile Ala Ser Met Gly Ile
                245   250   255

Tyr Val Phe Ser Lys Asp Val Met Leu Gln Leu Leu Arg Glu Gln Phe
                260   265   270

Pro Glu Ala Asn Asp Phe Gly Ser Glu Val Ile Pro Gly Ala Thr Ser
        275   280   285

Ile Gly Lys Arg Val Gln Ala Tyr Leu Tyr Asp Gly Tyr Trp Glu Asp
        290   295   300

Ile Gly Thr Ile Ala Ala Phe Tyr Asn Ala Asn Leu Gly Ile Thr Lys
305   310   315   320

Lys Pro Ile Pro Asp Phe Ser Phe Tyr Asp Arg Phe Ala Pro Ile Tyr
                325   330   335

Thr Gln Pro Arg His Leu Pro Pro Ser Lys Val Leu Asp Ala Asp Val
        340   345   350

Thr Asp Ser Val Ile Gly Glu Gly Cys Val Ile Lys Asn Cys Lys Ile
        355   360   365

Asn His Ser Val Val Gly Leu Arg Ser Cys Ile Ser Glu Gly Ala Ile
        370   375   380

Ile Glu Asp Ser Leu Leu Met Gly Ala Asp Tyr Tyr Glu Thr Glu Ala
385   390   395   400

Asp Lys Lys Leu Leu Ala Glu Lys Gly Gly Ile Pro Ile Gly Ile Gly
                405   410   415

Lys Asn Ser Cys Ile Arg Arg Ala Ile Ile Asp Lys Asn Ala Arg Ile
                420   425   430

Gly Asp Asn Val Lys Ile Leu Asn Ala Asp Asn Val Gln Glu Ala Ala
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Lys Asp Ala Leu Leu Pro Ser Gly Thr Val Ile
465   470   475

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<213>   zea mays

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Asp Ser Thr Cys Leu Asn Pro Gln Ala His Asp Ser Val Leu Gly Ile
        35   40   45

Ile Leu Gly Gly Gly Ala Gly Thr Arg Leu Tyr Pro Leu Thr Lys Lys
    50   55   60

Arg Ala Lys Pro Ala Val Pro Leu Gly Ala Asn Tyr Arg Leu Ile Asp
65   70   75   80

Ile Pro Val Ser Asn Cys Leu Asn Ser Asn Ile Ser Lys Ile Tyr Val
                85   90   95

Leu Thr Gln Phe Asn Ser Ala Ser Leu Asn Arg His Leu Ser Arg Ala
            100   105   110

Tyr Gly Ser Asn Ile Gly Gly Tyr Lys Asn Glu Gly Phe Val Glu Val
        115   120   125

Leu Ala Ala Gln Gln Ser Pro Asp Asn Pro Asn Trp Phe Gln Gly Thr
    130   135   140

Ala Asp Ala Val Arg Gln Tyr Leu Trp Leu Phe Glu Glu His Asn Val
145   150   155   160

Met Glu Phe Leu Ile Leu Ala Gly Asp His Leu Tyr Arg Met Asp Tyr
                165   170   175

Glu Lys Phe Ile Gln Ala His Arg Glu Thr Asn Ala Asp Ile Thr Val
            180   185   190

Ala Ala Leu Pro Met Asp Glu Lys Arg Ala Thr Ala Phe Gly Leu Met
        195   200   205

Lys Ile Asp Glu Glu Gly Arg Ile Ile Glu Phe Ala Glu Lys Pro Lys
    210   215   220

Gly Glu Gln Leu Lys Ala Met Met Val Asp Thr Thr Ile Leu Gly Leu

Asp Asp Val Arg Ala Lys Glu Met Pro Tyr Ile Ala Ser Met Gly Ile
                    245   250   255

Tyr Val Phe Ser Lys Asp Val Met Leu Gln Leu Leu Arg Glu Gln Phe
                    260   265   270

Pro Glu Ala Asn Asp Phe Gly Ser Glu Val Ile Pro Gly Ala Thr Ser
                275   280   285

Ile Gly Lys Arg Val Gln Ala Tyr Leu Tyr Asp Gly Tyr Trp Glu Asp
    290   295   300

Ile Gly Thr Ile Ala Ala Phe Tyr Asn Ala Asn Leu Gly Ile Thr Lys
305   310   315   320

Lys Pro Ile Pro Asp Phe Ser Phe Tyr Asp Arg Phe Ala Pro Ile Tyr
                    325   330   335

Thr Gln Pro Arg His Leu Pro Pro Ser Lys Val Leu Asp Ala Asp Val
                340   345   350

Thr Asp Ser Val Ile Gly Glu Gly Cys Val Ile Lys Asn Cys Lys Ile
                355   360   365

Asn His Ser Val Val Gly Leu Arg Ser Cys Ile Ser Glu Gly Ala Ile
                370   375   380

Ile Glu Asp Ser Leu Leu Met Gly Ala Asp Tyr Tyr Glu Thr Glu Ala
385   390   395   400

Asp Lys Lys Leu Leu Ala Glu Lys Gly Gly Ile Pro Ile Gly Ile Gly
                    405   410   415

Lys Asn Ser Cys Ile Arg Arg Ala Ile Ile Asp Lys Asn Ala Arg Ile
                420   425   430

Gly Asp Asn Val Lys Ile Leu Asn Ala Asp Asn Val Gln Glu Ala Ala
                435   440   445

Met Glu Thr Asp Gly Tyr Phe Ile Lys Gly Gly Ile Val Thr Val Ile
    450   455   460

Lys Asp Ala Leu Leu Pro Ser Gly Thr Val Ile
465   470   475

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cccttgacaa agaagcgtgc caagcctgca gtgccattgg gtgccaacta tagactgatt     240

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tttaactctg cttccctcaa ccgtcacctc tcaagagcct acgggagcaa cattggaggg     360

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aaacgtgcaa ctgcatttgg cctcatgaaa attgatgaag aagggaggat cattgagttt     660

gctgagaaac cgaaaggaga gcagttgaaa gcaatgatgg ttgacaccac catacttggc     720

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Asp Ser Gln Thr Tyr Leu Asn Pro Gln Ala His Asp Ser Val Leu Gly
         35              40              45

Ile Ile Leu Gly Gly Gly Ala Gly Thr Arg Leu Tyr Pro Leu Thr Lys
     50              55              60

Lys Arg Ala Lys Pro Ala Val Pro Leu Gly Ala Asn Tyr Arg Leu Ile
65              70              75              80

Asp Ile Pro Val Ser Asn Cys Leu Asn Ser Asn Ile Ser Lys Ile Tyr
             85              90              95

Val Leu Thr Gln Phe Asn Ser Ala Ser Leu Asn Arg His Leu Ser Arg
         100             105             110

Ala Tyr Gly Ser Asn Ile Gly Gly Tyr Lys Asn Glu Gly Phe Val Glu
         115             120             125

Val Leu Ala Ala Gln Gln Ser Pro Asp Asn Pro Asn Trp Phe Gln Gly
     130             135             140

Thr Ala Asp Ala Val Arg Gln Tyr Leu Trp Leu Phe Glu Glu His Asn
145             150             155             160

Val Met Glu Phe Leu Ile Leu Ala Gly Asp His Leu Tyr Arg Met Asp
             165             170             175

Tyr Glu Lys Phe Ile Gln Ala His Arg Glu Thr Asn Ala Asp Ile Thr
         180             185             190

Val Ala Ala Leu Pro Met Asp Glu Lys Arg Ala Thr Ala Phe Gly Leu
     195             200             205

Met Lys Ile Asp Glu Glu Gly Arg Ile Ile Glu Phe Ala Glu Lys Pro
210             215             220

Lys Gly Glu Gln Leu Lys Ala Met Met Val Asp Thr Thr Ile Leu Gly
225             230             235             240

Leu Asp Asp Val Arg Ala Lys Glu Met Pro Tyr Ile Ala Ser Met Gly
             245             250             255

Ile Tyr Val Phe Ser Lys Asp Val Met Leu Gln Leu Leu Arg Glu Gln
         260             265             270

Phe Pro Glu Ala Asn Asp Phe Gly Ser Glu Val Ile Pro Gly Ala Thr
         275             280             285

Ser Ile Gly Lys Arg Val Gln Ala Tyr Leu Tyr Asp Gly Tyr Trp Glu
     290             295             300

Asp Ile Gly Thr Ile Ala Ala Phe Tyr Asn Ala Asn Leu Gly Ile Thr
305             310             315             320
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Lys Lys Pro Ile Pro Asp Phe Ser Phe Tyr Asp Arg Phe Ala Pro Ile
            325   330   335

Tyr Thr Gln Pro Arg His Leu Pro Pro Ser Lys Val Leu Asp Ala Asp
            340   345   350

Val Thr Asp Ser Val Ile Gly Glu Gly Cys Val Ile Lys Asn Cys Lys
            355   360   365

Ile Asn His Ser Val Val Gly Leu Arg Ser Cys Ile Ser Glu Gly Ala
    370   375   380

Ile Ile Glu Asp Ser Leu Leu Met Gly Ala Asp Tyr Tyr Glu Thr Glu
385   390   395   400

Ala Asp Lys Lys Leu Leu Ala Glu Lys Gly Gly Ile Pro Ile Gly Ile
            405   410   415

Gly Lys Asn Ser Cys Ile Arg Arg Ala Ile Ile Asp Lys Asn Ala Arg
            420